International Journal of Agricultural
Science and Research (IJASR)
ISSN (P): 2250-0057; ISSN (E): 2321-0087
Vol. 11, Issue 2, Dec 2021, 141-148

MULTIVARIATE ANALYSIS IN BLACKGRAM (VIGNA MUNGO(L.) HEPPER)

SUJIT KUMAR DALAI, RUCHI BISHNOI & GAIBRIYAL M. LAL

Department of Genetics and Plant Breeding, Naini Institute of Agriculture,

Sam Higginbottom University of Agriculture, Technology and Sciences, Prayagraj, India

ABSTRACT

A study was carried out among thirty-five blackgram [Vigna mungo(L.) Hepper] genotypes, using Mahalanobis' D2 and principal component analysis for thirteen quantitative traits in randomized block design with three replication during zaid, 2021 at Naini Agricultural Institute, SHUATS, Prayagraj. The first 4 principal components showed >1 eigen value, which contributed 86.10 % of the total accumulated variability. PC1 explained 38.63% of the total variation, followed by 20.15%, 14.61% and 12.70%. The variable contributing most positively to PC 1 was seed yield per plant (0.43), to PC2 was seed index (0.49), to PC 3 was number of days to maturity (0.54) and to PC 4 were both days to 50% flowering and days to 50% pod setting (0.63; each). D2 statistics showed 5 clusters with highest intra-cluster distance were shown by Cluster I (63.71). Minimum inter-cluster distance was found between cluster II and III (118.73), followed by II and I (240.72) while, maximum inter-cluster distance was found between Cluster IV and V (2899.3), followed by III and V (1894.53), II and V (1670.81) and I and IV (1478.26). Also, maximal genetic divergence contribution was shown by seed yield per plant (17%), followed by harvest index (15%) and biological yield per plant (14%). Therefore, the characters that contribute to maximal divergence should be given more weight when determining clusters for the purpose of selecting parents for future hybridization.

KEYWORDS: Blackgram, Principle component analysis, Genetic diversity & D 2 - statistics

Received: Jun 23, 2021; **Accepted:** Jul 13, 2021; **Published**: Jul 26, 2021; **Paper Id.:** IJASRDEC202116

OriginalArticle

INTRODUCTION

Urdbean or Blackgram [Vigna mungo(L.)Hepper] is domesticated from Vigna mungo var. silvestris (Kaewwongwalet al., 2015). Blackgram has 20 to 25% of proteins which is thrice to that of cereals and 40 to 47% of starch. It is also a rich source of essential vitamins and minerals. Blackgram is said to have originated in the Indian subcontinent, according to Vavilov (1926).Its references have also been found in Vedic texts such as Kautilya's 'Arthasasthra' and in 'Charismata' which support to the presumption of its origin in India.

Though it is grown in different countries of South and South East Asia, India is the most important producer of blackgram. In India, the area, production and productivity of blackgram are 35.53 L-ha, 19.64 LT and 553 kg/ha, respectively. The major urdbean growing states of the country are Maharashtra, Andhra Pradesh, Rajasthan, Odisha, Tamil Nadu, Karnataka and Bihar. In Uttar Pradesh, blackgram is cultivated in 5.19 lakh hectare area with a production of 2.13 lakh tonne and productivity of 47.7 kg/ha. (Source: Directorate of Economics and Statistics, Ministry of Agriculture & farmers' welfare (DAC & FW), Govt. of India; 2020-2021).

The productivity of urd bean in India is very low due to several constraints viz., non-availability of quality seed of high yielding variety, seeds germinate in mature pod itself if there is rains at maturity time of crop and the crop is highly sensitive to high intensity rains etc., all such factors cause heavy losses in terms of yield. Thus, the

crop requires due attention to increase its production and productivity. However, pulses do possess enough potential for improvement. **(Swaminathan, 1973; Jain, 1975).**

Any crop development initiative must start with a thorough understanding of genetic diversity. Progenies from different parents are predicted to have a wide range of genetic variability, allowing for easier isolation of high-yielding cultivars. The D 2 statistic has been discovered to be a useful tool for measuring genetic diversity at the phenotypic level in a population when many characters are evaluated.

It should also be noted that the PCA can also be used to identify plant features that characterise the distinctiveness of prospective genotypes(Chakravortyetal., 2013).Principal component analysis (PCA) is used to reveal similarities between variables and identify genotypes, whereas cluster analysis is used to classify already unlabeled materials(Leonard and Peter, 2009).

While keeping the above facts under consideration, the present investigation on thirty-five black gram genotypes were carried out through multivariate analysis to identify genetically diverse genotypes and to identify traits which contribute to population variability.

MATERIALS AND METHODS

Inside the research farm of the Department of Genetics and Plant Breeding, SHUATS, Prayagraj, Uttar Pradesh, India, thirty-five genotypes of black-gram were examined during Zaid, 2021. Three replications were used in the randomised block design (RBD) experiment. Five one-meter rows with a 30 cm x l0cm gap represented each genotype. A 20:40:20 kg NPK/ha fertiliser dose was used, along with need-based plant protection measures.

The observations were made on the five plants chosen at random in each entry. Days to 50% flowering (DFF), days to 50% pod setting (DFPS), plant height (PH), number of primary branches per plant (NPBP), number of clusters per plant (NCP), number of pods per plant (NPP), number of seeds per plant (NSP),Pod length (PL), days to maturity (DM), seed index (SI), biological yield (BY), harvest index (HI) and seed yield per plant (SY) were among the thirteen quantitative features observed.

The data were subjected to statistical analysis using Mahalanobis' D 2 statistic (Mahalanobis, 1936) and Principal Component Analysis (PCA) (Pearson, 1901). Tocher's approach was used to divide the genotypes into separate clusters as described by (Rao, 1952).Results of PCA and cluster analysis are discussed here.

RESULTS AND DISCUSSIONS

Based on the pooled analysis, the ANOVA suggests that there is a significant difference for almost all the characters at 1% level of significance except days to 50% flowering, days to 50% pod setting, number of days to maturity and seed index. This indicates that the material has adequate genetic variability to support the breeding programme for improving the seed yield of blackgram.

A perusal of mean performance among 35 black-gram genotypes recorded that KU-48 genotype showed highest yield per plant (9.39 g), followed by LBG-752 (6.24g), BARABANKI (3.94 g) and PLU-1050 (3.84g). KU-48 also showed highest mean performance for the characters viz., number of clusters per plant, number of pods per plant, biological yield per plant and harvest index. Also, the performance of KU-48 for all the characters, except days to maturity was higher than the check Sekhar-2. Nine genotypes viz., IPU-94-2, PLU-86-C, TAU-1, AKU-11-21, VBG-11-016, KU-88-31-2, KU-96-7,

IPU-99-16 and IPH-98-1 performed less than the check, whereas rest of the genotypes showed higher performance than Sekhar-2, for various characters, especially for yield per plant. Therefore, these genotypes may be promoted for cultivation as well as in future breeding programme to develop superior varieties for sustainable agricultural production.

In this investigation, PCs with eigen values greater than one and that explained at least 5% of the variation in the data were evaluated. The first principal component absorbs and accounts for the greatest proportion of total variability in the set of all variables, while the following components account for decreasing amounts of variance. In the current investigation, the same pattern was seen. Four (4) of the 13 principal components (PCs) had an Eigen value greater than 1.00 and 86.10 percent cumulative variability among the qualities investigated. As a result, these four PCs were given special consideration for additional explanation.

The first principal component accounted for 38.63% of the total variance, followed by 20.15%, 14.61% and 12.70%. The variable contributing most positively to PC 1 was seed yield per plant (0.43), to PC2 was seed index (0.49), to PC 3 was number of days to maturity (0.54) and to PC 4 were both days to 50% flowering and days to 50% pod setting (0.63; each). These similar outcomes have been recorded by earlier workers (Sridhar et al., 2020 and Thirumalai et al., 2020). Similar usage of PCA for obtaining 2D diagrams and in turn to understand the genetic diversity was also employed by Ayesha et al.,(2021), to indicate that "the successful hybrid combination to obtain superior hybrids or transgressive segregants depending on the gene action guiding different traits".

The genetic diversity among 35 genotypes was measured by employing D 2 statistics and Tocher's method was used to divide the data into five clusters as given by Rao (1952). Cluster I constitutes of 31 genotypes, indicating that crossing among the genotypes in this cluster may give transgressive segregants, and cluster II, III, IV and V all constitutes of single genotype. The single genotype present in the cluster II, III, IV and V indicates that it could be more divergent from the other genotypes and the crossing of them with the genotypes from other clusters could provide heterosis for some of the most essential traits.

The fact that the inter cluster distance was greater than the intra cluster distance suggested a significant level of genetic diversity across the genotypes analysed. Zero intra cluster distance was found for cluster II, III, IV and V, while in Cluster I it was 63.71. Cluster II and III had the smallest intercluster distance (118.73), followed by II and I (240.72),indicating a close association. These genotypes can also be utilised in breeding programmes to create biparental crosses between the most diverse and the closest groups in order to disrupt the unfavourable correlations between yield and its related characteristics. Cluster IV and V had the greatest inter-cluster distance (2899.3), followed by III and V (1894.53), II and V (1670.81) and I and IV (1478.26). This is clearly indicated that the genotypes in these clusters span a wide range of genetic diversity. It is therefore suggested that the superior genotypes from various clusters could be used as parents in a hybridization programme. Maximum contribution to genetic divergence was shown by seed yield per plant (17%), followed by harvest index (15%) and biological yield per plant (14%). Thirumalai et al., 2020 also observed similar findings.Characters that contribute to maximal divergence should be given more weight when determining clusters for the purpose of selecting parents for future hybridization.

With the use of principal component and principle factor analysis, the current study successfully classified genotypes based on genetic divergence, and the comprehension of many interrelated qualities involved in genetic control of grain output has increased. As a result, these findings will undoubtedly contribute to the development of a well-defined approach based on the evaluation and characterization of genetic variation in rice, which can be applied to a variety of

breeding programmes depending on their specific goals.

CONCLUSIONS

From the present investigation, it is concluded that among 35 genotypes of black-gram on the basis of mean performance KU-48 was found to be superior grain yield over check. It showed high harvest index, number of pods per plant and number of clusters per plant. Results of PCA revealed that principle component 1, 2, 3 and 4 showed 86.10% to variance, among which PC 1 solely showed 38.63% to genetic variance. The character seed yield per plant has highest contribution to genetic variance via PC 1. From D 2 analysis, it can be estimated that Cluster I has the greatest intra-cluster separation, whereas Clusters IV and V have the greatest inter-cluster separation. While cluster IV is highest performing among clusters. Lastly, the contribution of seed yield per plant is highest for genetic divergence. As a result, these characteristics should be given top priority while selecting enhancement yield in blackgram.

Table 1: Analysis of variance for 13 Quantitative Characters of Black-Gram

Sl.No.	Characters	MeanSumofSquare		
		Replication (d.f=2)	Treatment (d.f=34)	Error (d.f=68)
1	Days to 50% flowering	0.6	5.62	7.18
2	Days to 50% pod setting	6.2	4.79	9.63
3	Plant height	2.25	23.79**	3.02
4	Number of Primary branches	0.78*	1.89**	0.22
5	Number of clusters per plant	1.72*	5.01**	0.38
6	Number of days to maturity	42.18*	17.26	10.87
7	Number of pods per plant	7.86*	82.18**	2.13
8	Number of seeds per pod	0.79**	1.24**	0.06
9	Pod length	0.01	0.17**	0.005
10	Biological yield per plant	0.03**	48.63**	0.003
11	Seed Index	0.40**	0.05	0.05
12	Harvest Index	11.69	108.18**	19.39
13	Seed yield per plant	1.42	6.41**	0.09

Table 2: PCA of 35 Genotypes of Blackgram for 13 characters

	1	2	3	4	5
Eigene Value (Root)	5.73	2.12	1.63	1.01	0.69
% Var. Exp.	44.11	16.33	12.56	7.78	5.34
Cum.Var.Exp.	44.11	60.44	73.00	80.78	86.12
Days to 50% flowering	0.05	-0.54	-0.30	0.20	0.28
Days to 50% pods setting	-0.002	-0.49	-0.34	0.39	-0.15
Plant height (cm)	0.33	0.10	0.04	0.02	-0.29
Number of primary branches	0.21	-0.18	-0.43	-0.28	0.29
Number of clusters per plant	0.39	-0.06	0.10	-0.01	0.12
Number of days to maturity	0.21	-0.43	0.24	-0.07	-0.29
Number of pods per plant	0.38	-0.05	0.13	-0.03	0.32
Number of seeds per pod	0.28	0.22	-0.16	0.13	-0.60
Pod length (cm)	0.28	0.17	-0.11	0.42	-0.09
Biological yield per plant (g)	0.34	-0.13	0.34	-0.08	0.08
Seed Index	0.07	-0.25	-0.34	-0.70	-0.29
Harvest index(%)	0.20	0.24	-0.48	0.09	0.14
Seed yield per plant(g)	0.40	-0.0048	0.07	-0.04	0.17

Table 3: Composition of D² Clusters for 35 Blackgram Genotypes in Pooled Analysis

Clusters	Number of genotypes	Name of genotypes
I	31	LBG-648, SNTP-02, SPS-40, KC-153, SPS-42, IPU-92-2,KU-99-16, IPU-1070, PLU-86- C, PU-11-14, TAU-1, AKU-11-14, VBG-11-016, PLU-1050, L-6, KU-88-31-2, IPU-94-1, ADT-3, IC-106-176, AKU-16-03, KU-96-7, LBG-20, LBG-645, PDV-2, BARABANKI, PLU-1016, IPU-99-16, VBN-08, UK-10, IPH-98-1, SHEKHAR-2(CHECK)
II	1	KU-42
III	1	LBG-752
IV	1	KU-48
V	1	PLU-429

Table 4: Cluster Distances

Cluster Distances					
	Cluster1	**Cluster2**	**Cluster3**	**Cluster4**	**Cluster5**
Cluster 1	63.71				
Cluster 2	240.72	0			
Cluster 3	537.02	118.73	0		
Cluster 4	1478.26	659.66	261.9	0	
Cluster5	1352.66	1670.81	1894.53	2899.3	0

Table 5: Cluster Means: Tocher Method

	Cluster 1	**Cluster 2**	**Cluster 3**	**Cluster 4**	**Cluster 5**
Days to 50% flowering	52.19	55	**51**	53	**51**
Days to 50% pods setting	58.52	59	**57**	58	60
Plant height(cm)	18.35	19.6	**27.2**	23.8	20
Number of primary branches per plant	3.21	3	4	**4.4**	3
Number of clusters per plant	3.48	5.6	6.8	**8**	4.2
Number of days to maturity	**76.64**	81	81	81	81
Number of pods per plant	11.55	19	24.4	**35.8**	11.6
Number of seeds per pod	5.33	5	**6.4**	**6.4**	5.8
Pod length (cm)	3.79	3.86	3.96	**4.22**	3.72
Biological yield per plant (g)	**9.13**	18.6	18.2	24.2	12.8
Seed Index	4.02	4.1	4	4.1	**4.2**
Harvest index(%)	27.75	20.94	34.31	**38.81**	22.07
Seed yield perplant (g)	2.5	3.89	6.25	**9.39**	2.82

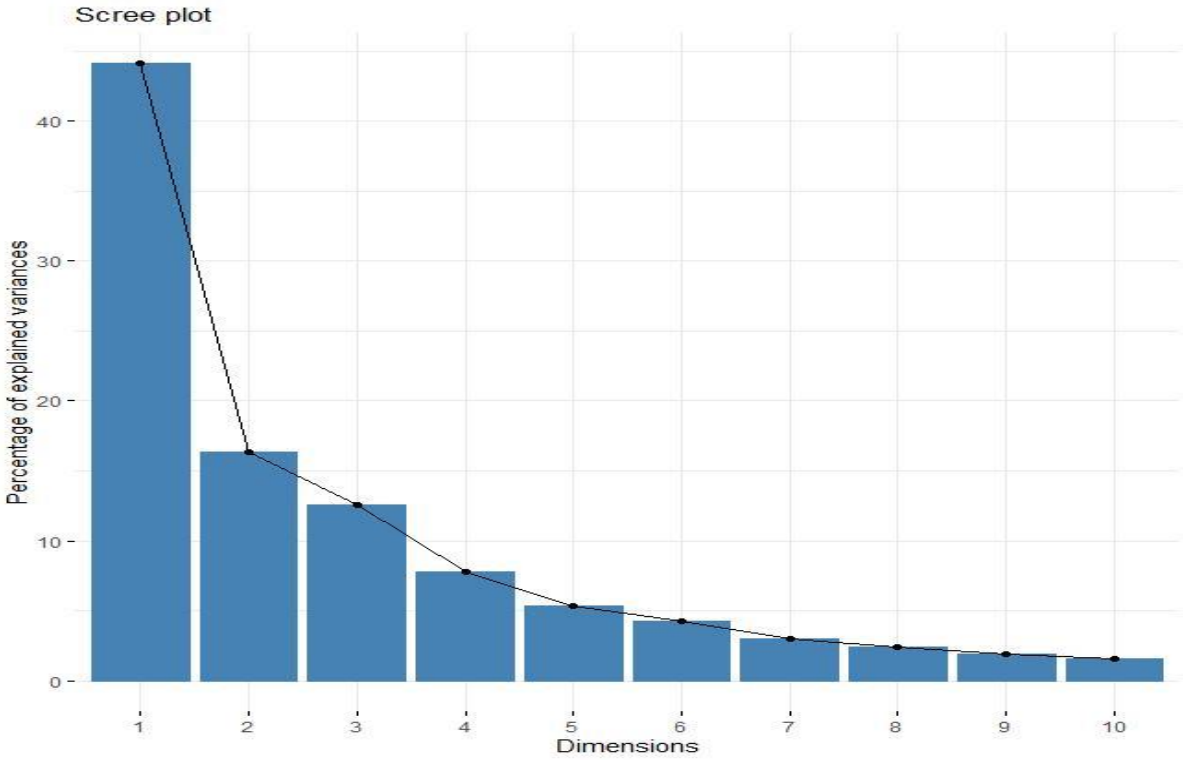

Figure 1: Screen plot showing Eigen Value Variation

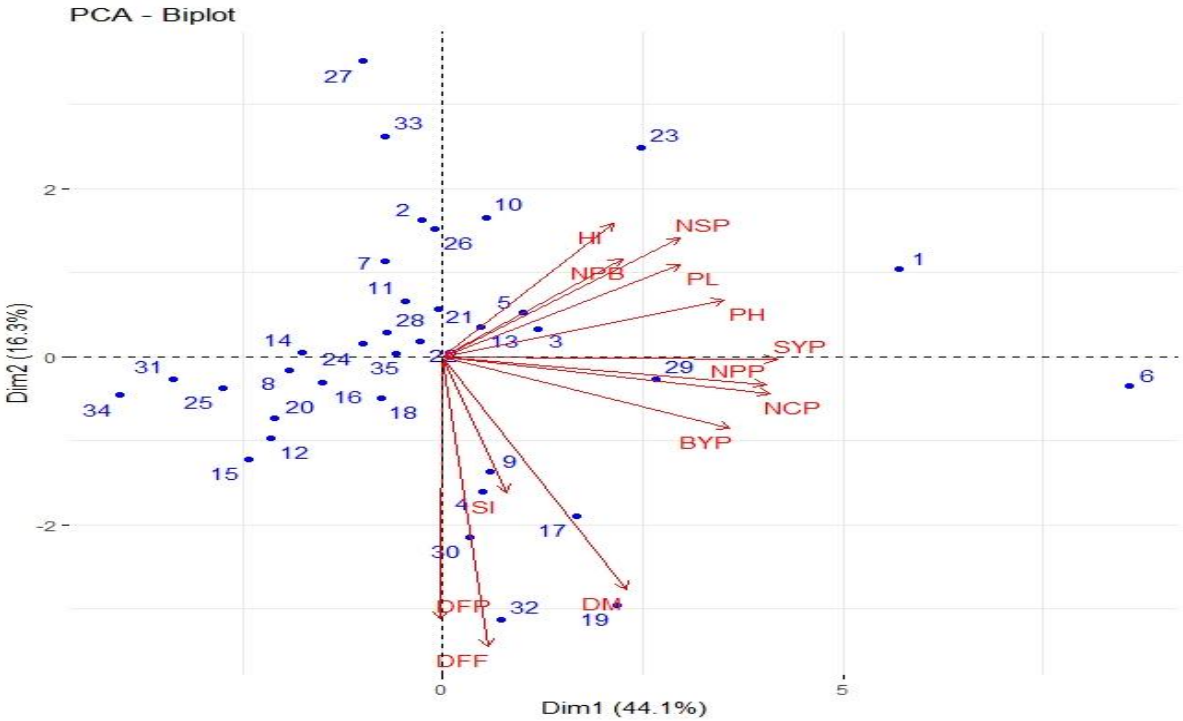

Figure 2: Distribution of various traits and Genotypes across Two Components

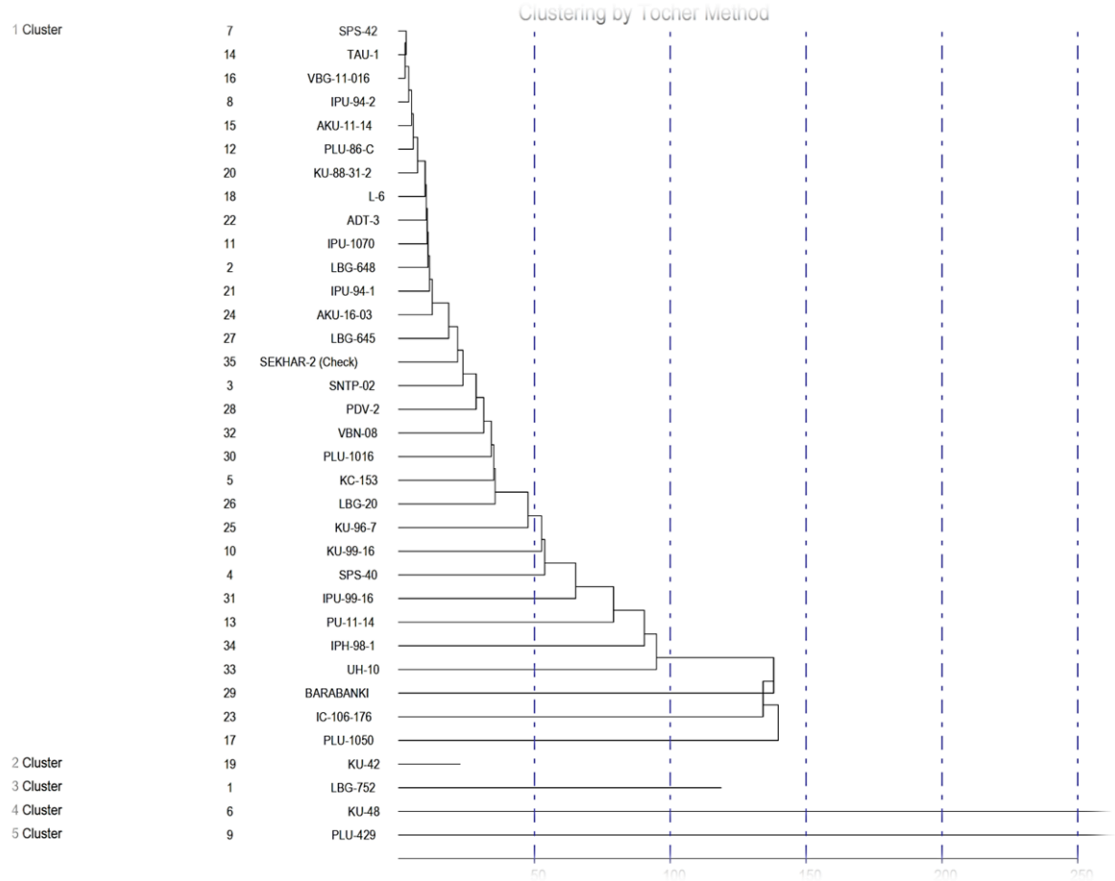

Figure 3: Clustering by Tocher Method

REFERENCES

1. *Ayesha, Md., Babu, D.R., Lal, A.P.R., Ahmed Md and Kumar, V.M. (2021).Principal components of genetic diversity in black gram[Vignamungo (L.)Hepper].The Pharma Innovation Journal 2021; 10(4): 250-253*
2. *Banfield, C. F.(1978).Principal component analysis for genstat. J.Static. Comput. Simul.6:211-222*
3. *Carroll, J.B. (1953).An analytical solution for approximating simple structure in factor analysis. Psychometrika, 18, 23-28.*
4. *Chakravorty, A., Ghosh, P.D., and Sahu, P.K. (2013).Multivariate analysis of landraces of rice of West Bengal. American journal of Experimental Agriculture.3(1):110-123.*
5. *Geethanjali, Anuradha, C., and Suman (2015).Genetic Diversity for Yield and its Components in Black gram (VignamungoL.). vol. 4, Issue: 8:2277 – 8179.*
6. *Ghafoor, A., Sharif, A., Ahmed, Z., Zahid, M. A. and Rabbani, M. A.(2001).Genetic diversity in blackgram [Vignamungo(L.)Hepper].Field Crops Research, 69: 183 – 190*
7. *Goldchild, N.A. and Boyd, W.J.R. (1975) Regional and temporal variation in Wheat yield in Western Australia and their implications in plant breeding. Australian Journal of Agricultural Research, 26, 209.*
8. *Gupta, S., Shivkumar, Singh B. B. and Subhashchandra (2005) Contribution of different morphological and yield related traits to urd bean diversity. Indian Journal of Pulses Research, 18(1): 14-16.*
9. *Jeberson, M.S., Shashidhar, K. and Singh, A.K. (2019).Genetic variability, principal component and cluster analyses in black gram under Foot-hills conditions of Manipur. Legume Research, 42(4): 454-460.*

10. Kaiser, H.F. (1958). The varimax criterion for analytic rotation in factor analysis. Psychometrika, 23, 187..
11. Kamannavar, P. Y., Revanappa, S.B., Vijaykumar, A. G.,Basamma, K. and Ganajaxi (2016).Nature of genetic diversity for seed yield and its component traits in urdbean [Vignamungo(L.) Hepper].Indian J. Agric. Res., 50(1): 96-98.
12. Kaufman, L. and Rousseeuw, P.J. (2009).Finding groups in data: an introduction to cluster analysis. John Wiley and Sons.
13. Leonard, K. and Peter, R.J. (2009).Finding Groups in data: An Introduction to cluster Analysis, 344.
14. Mahalanobis P.C. (1928).On the generalised distance in statistics. Proc. Nat. Acad. Sci. 19:201-208.
15. Mohanlal, VA., Saravanan, K. and Sabesan, T. (2018).Multivariate analysis in blackgram (Vignamungo(L.) hepper) genotypes. Journal of Pharmacognosy and Phytochemistry; 7(6): 860-863
16. Morrison, D.F. (1978). Multivariate Statistical Methods. McGraw-Hill International Book Co., London
17. Peeters, J. and Martinelli, J.(1989).Hierarchical cluster analysis as a tool to manage variation in germplasmcollections. Theoretical and Applied Genetics.78: 42-48.
18. Rajasekhar, D., Yadav, B.N.P., Hemalatha, K., Ranjithkumar, G., and Lal, G.M. (2020) multivariate analysis in blackgram (Vignamungo (L.)Hepper) 15(2):257-259.
19. Rao, C.R. (1952).Advanced statistical method in biometrical research. John Wiley and sons Inc., New york.
20. Reddy, A.K., Priya M.S., Reddy, D.M. and Reddy, B.R. (2018) Genetic Divergence Studies in Blackgram (Vignamungo (L.)Hepper).Int. J. Pure App. Biosci.6 (5): 232-237.
21. Sokal, R.R., Howell, V.D. and Rohlf, F.J. (1961) Factor analytical procedures in biological model. University of Kansas Science Bulletin, 42, 1099-1121.
22. Sridhar, V., B.V. Vara Prasad, D. Shivani and S. SrinivasaRao (2020). Genetic Divergence Studies for Yield Components in Blackgram (Vignamungo L.) Genotypes.Int. J. Curr. Microbiol. App. Sci., 9(01): 1816-1823.
23. Thirumalai, R. and Murugan, S. (2020).Multivariate analysis in blackgram (Vignamungo (L.)Hepper) genotypes for mungbean yellow mosaic virus (mymv) resistance. Plant Archives, 20 (1): 2473-2480
24. Veni, K., Murugan, E., Mini, M.L., Vanniarajan, C. and Radhamani, T. (2016). Genetic relationship between yield and battering quality in blackgram (VignamungoL.), Legume Research, 39(3): 355-358.
25. Adawy, SAMI S., and MOHAMED AM Atia. "A multidisciplinary molecular marker approaches to assess the genetic diversity in Egyptian date palm."; J. of Biotechnology and Research 4 : 1-12.
26. Sangin, Pattamon, and Sirilak Khotsuwan. "Development of Novel Est-Ssr markers to assess genetic diversity in Curcuma Longa L" International Journal of Bio-Technology and Research (IJBTR) 9.2 : 1-8.
27. SANGANI, KINJAL. "Optimization of DNA isolation and analysis of genetic variability in medicinal plant cissus by rapd-pcr technique"; International Journal of Applied and Natural Sciences (IJANS) 6.5 : 15-22.
28. Amrata, Sharma, and Arora Asha. "Study of Genetical Diversity of Mahseer (Tor Tor) from Rana Pratap Sagar Dam, Kota (Rajasthan) India"; International Journal of Applied and Natural Sciences (IJANS): 2319-4014.